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length and altered to have the following composition: 15-35 mole % lysine, 8-15 mole % methionine, 13-25 mole % threonine, 6-12 mole % tryptophan, 12-20 mole % isoleucine or combinations thereof; wherein the % sequence identity is based on the entire sequence and is determined by BLAST 2.0.

54. (once amended) The polypeptide of claim 9, wherein the polypeptide is altered to have 8-15 mole % methionine.

55. (once amended) The polypeptide of claim 9, wherein the polypeptide is altered to have 13-25 mole % threonine.

59. (once amended) A polypeptide with at least 60% sequence identity to the polypeptide of SEQ ID NO: 2 and comprising greater than 50 amino acids in length and comprising about 15 mole % or more lysine based on the total number of amino acid residues; wherein the % sequence identity is based on the entire sequence and is determined by BLAST 2.0.

60. (once amended) The polypeptide of Claim 59, further comprising about 20 mole % or more lysine based on the total number of amino acid residues.

Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached page is captioned, "Version With Markings to Show Changes Made."